IN THE CLAIMS:

Please amend claims 3-7 and 14-15 as follows:

1-2. (Cancelled)

3. (Currently Amended) A method for displaying gene expression data in comparing gene expression levels of a plurality of ~~common~~ genes [[for]] found in different ~~samples~~ Samples A, B, C, comprising:

calculating a first ratio b/a of a gene expression level b of [[each]] one of said ~~common~~ plurality of genes for the Sample B with respect to a gene expression level a of said one of said plurality of genes for the Sample A for each of [[a]] said plurality of genes in a first experiment;

calculating a second ratio c/A of a gene expression level c of said one of said plurality of genes for the Sample C with respect to a gene expression level A of said one of said plurality of genes for the Sample A for said each of [[a]] said plurality of genes in a second experiment;

obtaining a dataset of gene expression levels for the Samples B, C, A expressed as (b/a, c/A, 1) for said each of [[a]] said plurality of genes;

calculating a first magnitude r of said dataset expressed as $r = \text{sqrt}\{(b/a)^2 + (c/A)^2 + 1\}$; and

displaying a mark of a first product of the first ratio and K/r, a second product of the second ratio and the K/r, and the K/r on a coordinate position with respect to x-, y- and z-axes on a surface of a sphere for said each of [[a]] said plurality of genes, K being a radius of the sphere, to thereby compare gene expression levels of [[the]] said plurality of ~~common~~ genes [[for]] found in the samples A, B, C.

4. (Currently Amended) A method for displaying gene expression data according to claim 3, further comprising: calculating a second magnitude R of said dataset expressed as $R = \text{sqrt}\{(b^2 + c^2 + (a + A)^2)$ displaying a mark of a third product of the first ratio and R/r, a fourth product of the second ratio and the R/r, and the R/r on a coordinate positions with respect to x-, y- and z-axes for said each of [[a]] said plurality of ~~common~~ genes.

5. (Currently Amended) A method for displaying gene expression data according to claim 3, further comprising: performing a clustering analysis on the displayed marks for said plurality of ~~common~~ genes on the sphere; and marking at least one gene group obtained by the clustering analysis as a region on the sphere.

6. (Currently Amended) A method for displaying gene expression data according to claim 4, further comprising: performing a clustering analysis on the displayed magnitude coordinate positions inside the sphere for said plurality of ~~common~~ genes; and marking at least one gene group obtained by the clustering analysis as a region inside the sphere.

7. (Currently Amended) A method for displaying gene expression data according to claim 3, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of [[a]] said plurality of ~~common~~ genes in conjunction with a direction of changes of the coordinate positions with time in the displaying step.

8. (Previously Presented) A method for displaying gene expression data according to claim 5, wherein the expression level data is data in a time series, and said region is displayed based on respective time points in conjunction with a direction of changes of said region with time in the displaying step.

9-13. (Cancelled)

14. (Currently Amended) A method for displaying gene expression data according to claim 4, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of [[a]] said plurality of ~~common~~ genes in conjunction with a direction of changes of the coordinate positions with time in the displaying step.

15. (Currently Amended) A method for displaying gene expression data according to claim 5, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of [[a]] said plurality of ~~common~~ genes

in conjunction with a direction of changes of the coordinate positions with time in the displaying step.

16. (Original) A method for displaying gene expression data according to claim 6, wherein the expression level data is data in a time series, and said region is displayed based on respective time points in conjunction with a direction of changes of said region with time in the displaying step.

17. (Cancelled)